

IN THE CLAIMS:

Please amend the claims as indicated below:

1. (Currently amended) A computer-implemented method for characterizing gene expression, the method comprising executing, via a computer, the following steps of:

5 determining a plurality of gene expression signals for a gene, wherein said plurality of gene expression signals comprise control data and phenotype data;

transforming said control data, wherein transforming said control data comprises transforming a probability density distribution for said control data to a uniform probability density for said control data, wherein said transforming results in transformed control data having a uniform distribution of said gene expression signals within a selected interval in said control data, and wherein said transformed control data is applied to corresponding phenotype data to convert said corresponding phenotype data to one or more transformed phenotype values;

10 using said one or more transformed phenotype values to determine one or more gene expression patterns by searching said one or more transformed phenotype values for one or more patterns, wherein searching comprises using a pattern-finding algorithm to determine the one or more gene expression patterns;

15 generating a model for a probability density function of an expression level for each of the one or more gene expression patterns of the phenotype data;

20 characterizing gene expression of an unknown sample by using the model for the probability density function of the expression level for each of the one or more gene expression patterns of the phenotype data to determine determining one or more gene expression patterns for said unknown sample and comparing said one or more gene expression patterns of said unknown sample with said one or more gene expression patterns that characterize said control data and said phenotype data to classify said unknown sample as similar to either said control data or said phenotype data or neither; and

outputting said characterization to a user.

2. (Previously presented) The method of claim 1, further comprising the step of transforming gene expression signals of an additional sample.

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3. (Previously presented) The method of claim 1, wherein the step of transforming comprises the steps of:

determining a function that approximates a distribution of the plurality of gene expression signals for the gene; and

10 using the function to transform said plurality of gene expression signals, wherein said transformed gene expression signals have a uniform distribution of said gene expression signals within a selected interval in said control data.

4. (Canceled)

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17. (Currently amended) A system comprising:

a memory that stores computer-readable code; and

15 a processor operatively coupled to the memory, the processor configured to implement the computer-readable code, the computer-readable code configured to:

determine a plurality of gene expression signals for a gene, wherein said plurality of gene expression signals comprise control data and phenotype data;

20 transform said control data, wherein transforming said control data comprises transforming a probability density distribution for said control data to a uniform probability density for said control data, wherein said transforming results in transformed control data having a uniform distribution of said gene expression signals within a selected interval in said control data, and wherein said transformed control data is applied to corresponding phenotype data to convert said corresponding phenotype data to one or more transformed phenotype values;

25 use said one or more transformed phenotype values to determine one or more gene expression patterns by searching said one or more transformed phenotype values for one or more patterns, wherein searching comprises using a pattern-finding algorithm to determine the

one or more gene expression patterns;

generate a model for a probability density function of an expression level for each of the one or more gene expression patterns of the phenotype data;

5 characterize gene expression of an unknown sample by using the model for the probability density function of the expression level for each of the one or more gene expression patterns of the phenotype data to determine determining one or more gene expression patterns for said unknown sample and comparing said one or more gene expression patterns of said unknown sample with said one or more gene expression patterns that characterize said control data and said phenotype data to classify said unknown sample as similar to either said control data or said

10 phenotype data or neither; and

 output said characterization to a user.

18. (Previously presented) The system of claim 17, wherein the computer-readable code is further configured to transform gene expression signals of an additional sample.

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19. (Previously presented) The system of claim 17, wherein the computer-readable code is further configured, during the step of deriving, to perform the steps of:

 determine a function that approximates a distribution of the plurality of gene expression signals for the gene; and

20 use the function to transform said plurality of gene expression signals, wherein said transformed gene expression signals have a uniform distribution of said gene expression signals within a selected interval in said control data.

20. (Canceled)

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21. (Canceled)

22. (Cancelled)

23. (Currently amended) An article of manufacture comprising:

5 a computer readable medium having computer readable code means embodied thereon, the computer readable program code means comprising:

a step to determine a plurality of gene expression signals for a gene, wherein said plurality of gene expression signals comprise control data and phenotype data;

10 a step to transform said control data, wherein transforming said control data comprises transforming a probability density distribution for said control data to a uniform probability density for said control data, wherein said transforming results in transformed control data having a uniform distribution of said gene expression signals within a selected interval in said control data, and wherein said transformed control data is applied to corresponding phenotype data to convert said corresponding phenotype data to one or more transformed phenotype values;

15 a step to use said one or more transformed phenotype values to determine one or more gene expression patterns by searching said one or more transformed phenotype values for one or more patterns, wherein searching comprises using a pattern-finding algorithm to determine the one or more gene expression patterns;

20 a step to generate a model for a probability density function of an expression level for each of the one or more gene expression patterns of the phenotype data;

25 a step to characterize gene expression of an unknown sample by using the model for the probability density function of the expression level for each of the one or more gene expression patterns of the phenotype data to determine determining one or more gene expression patterns for said unknown sample and comparing said one or more gene expression patterns of said unknown sample with said one or more gene expression patterns that characterize said control data and said phenotype data to classify said unknown sample as similar to either said

control data or said phenotype data or neither; and

a step to output said characterization to a user.

24. (Previously presented) The article of manufacture of claim 23, wherein the computer-
5 readable code means further comprises a step to transform gene expression signals of an
additional sample.

25. (Previously presented) The article of manufacture of claim 23, wherein the computer-
readable code means is further configured, during the step of deriving, to perform:

10 a step to determine a function that approximates a distribution of the plurality of
gene expression signals for the gene; and

a step to use the function to transform said plurality of gene expression signals,
wherein said transformed gene expression signals have a uniform distribution of said gene
expression signals within a selected interval.

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26. (Canceled)

27. (Canceled)

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29. (Previously presented) The method of claim 1, wherein the selected interval comprises
an interval between 0 and 1.